REMARKS

Claims 104-119 presently appear in this case. No claims have yet been acted upon on the merits. The official action of August 7, 2006, has now been carefully studied. The claims have been subject to a restriction requirement. Reconsideration and withdrawal of the restriction requirement to the extent requested below and examination of all the claims now present in the case are hereby respectfully urged.

The examiner has made a unity of invention restriction requirement. Among the groups are Group II, drawn to a polypeptide fragment; Group III, drawn to a nucleic acid, vector or host cell; and Group V, drawn to an antibody. The examiner states that the groups do not relate to a single general inventive concept under PCT Rule 13.1 because they lack the same or corresponding special technical feature. The examiner states that claim 22 lacks novelty as being anticipated by Sugamura. The examiner states that Sugamura teaches anti-human cγc antibodies capable of inhibiting the binding between IL-2 receptor β and γ chains. This unity of invention restriction requirement is respectfully traversed.

The claims have now been amended to specify that the polypeptide is capable of binding to NIK and comprises the intracellular domain of cγc or a fragment, variant, derivative or circularly permutated derivative thereof that retains the ability to bind NIK. The claim specifies that the polypeptide contains no more of the sequence of cγc than the intracellular domain thereof.

Thus, the present claims do not exclude the extracellular domain of cγc.

Sugamura discloses the full cγc molecule and the portion cited by the examiner at column 10, lines 46-56, relates to ligand interaction, i.e., extracellular events. The antibodies of Sugamura do not bind to the intracellular domain. Thus, nothing in Sugamura anticipates or makes obvious any aspect of the presently claimed invention.

The method of using claims and small molecule claims have now been deleted without prejudice toward the continuation of prosecution thereof in a divisional application. The remaining claims include what the examiner had designated as Groups II, III and V. In order to be responsive, applicant hereby elects Group II, drawn to a polypeptide fragment. Claims 104-111 read on the elected group. However, in view of the fact that all of the present claims share the same or corresponding special technical feature, the restriction requirement should be withdrawn and all of the present claims examined.

The examiner states that in addition to an election of one of the above listed inventions, applicant must elect one corresponding SEQ ID NO. to be searched. In order to be responsive applicant hereby elects the 41MDD polypeptide, which is residues 329-369 of SEQ ID NO: 22.

It has been noted that the present specification includes sequences that are not identified by SEQ ID NOs. In order to facilitate description of these sequences, applicant has added to the sequence listing SEQ ID NO: 22, which is the full

length 369 amino acid cγc protein. Note that the sequences originally filed included the sequence of residue 1-357 of cγc (originally filed SEQ ID NO: 20), as well as the 12 amino acids at the C-terminus of cγc, i.e., residues 358-369 (SEQ ID NO: 3). Thus, the full sequence of 1-369 appeared in the specification as originally filed and new SEQ ID NO: 22 contains no new matter. The specification and claims have now been amended to refer to the various fragments as being fragments of SEQ ID NO: 22, so as to avoid confusion. Furthermore, the mutants appearing in Table 3 have been given their own SEQ ID NOs, 23-27. Many of these mutants are now being claimed.

Applicants have added into the present specification a new paper copy Sequence Listing section according to 37 C.F.R. §1.821(c) as new pages. Furthermore, attached hereto is a file (either on a 3½" disk or in an online text file) containing the "Sequence Listing" in computer readable form in accordance with 37 C.F.R. §1.821(e).

Applicants have amended the specification to insert SEQ ID Nos, as supported in the present specification.

The following statement is provided to meet the requirements of 37 C.F.R. §1.825(a) and 1.825(b).

I hereby state, in accordance with 37 C.F.R. §1.825(a), that the amendments included in the substitute sheets of the sequence listing are believed to be supported in the application as filed and that the substitute sheets of the sequence listing are not believed to include new matter.

I hereby further state, in accordance with 37 C.F.R. §1.825(b), that the attached copy of the computer readable form is the same as the attached substitute paper copy of the sequence listing.

Under U.S. rules, each sequence must be classified in <213> as an "Artificial Sequence", a sequence of "Unknown" origin, or a sequence originating in a particular organism, identified by its scientific name.

Neither the rules nor the MPEP clarify the nature of the relationship which must exist between a listed sequence and an organism for that organism to be identified as the origin of the sequence under <213>.

Hence, counsel may choose to identify a listed sequence as associated with a particular organism even though that sequence does not occur in nature by itself in that organism (it may be, e.g., an epitopic fragment of a naturally occurring protein, or a cDNA of a naturally occurring mRNA, or even a substitution mutant of a naturally occurring sequence). Hence, the identification of an organism in <213> should not be construed as an admission that the sequence *per se* occurs in nature in said organism.

Similarly, designation of a sequence as "artificial" should not be construed as a representation that the sequence has no association with any organism. For example, a primer or probe may be designated as "artificial" even though it is necessarily

complementary to some target sequence, which may occur in nature. Or an "artificial" sequence may be a substitution mutant of a natural sequence, or a chimera of two or more natural sequences, or a cDNA (i.e., intron-free sequence) corresponding to an intron-containing gene, or otherwise a fragment of a natural sequence.

The Examiner should be able to judge the relationship of the enumerated sequences to natural sequences by giving full consideration to the specification, the art cited therein, any further art cited in an IDS, and the results of his or her sequence search against a database containing known natural sequences.

Accordingly, reconsideration and withdrawal of the restriction requirement and prompt examination on the merits and allowance of the claims now present in the case is earnestly solicited.

Respectfully submitted,

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